

Fig. 1

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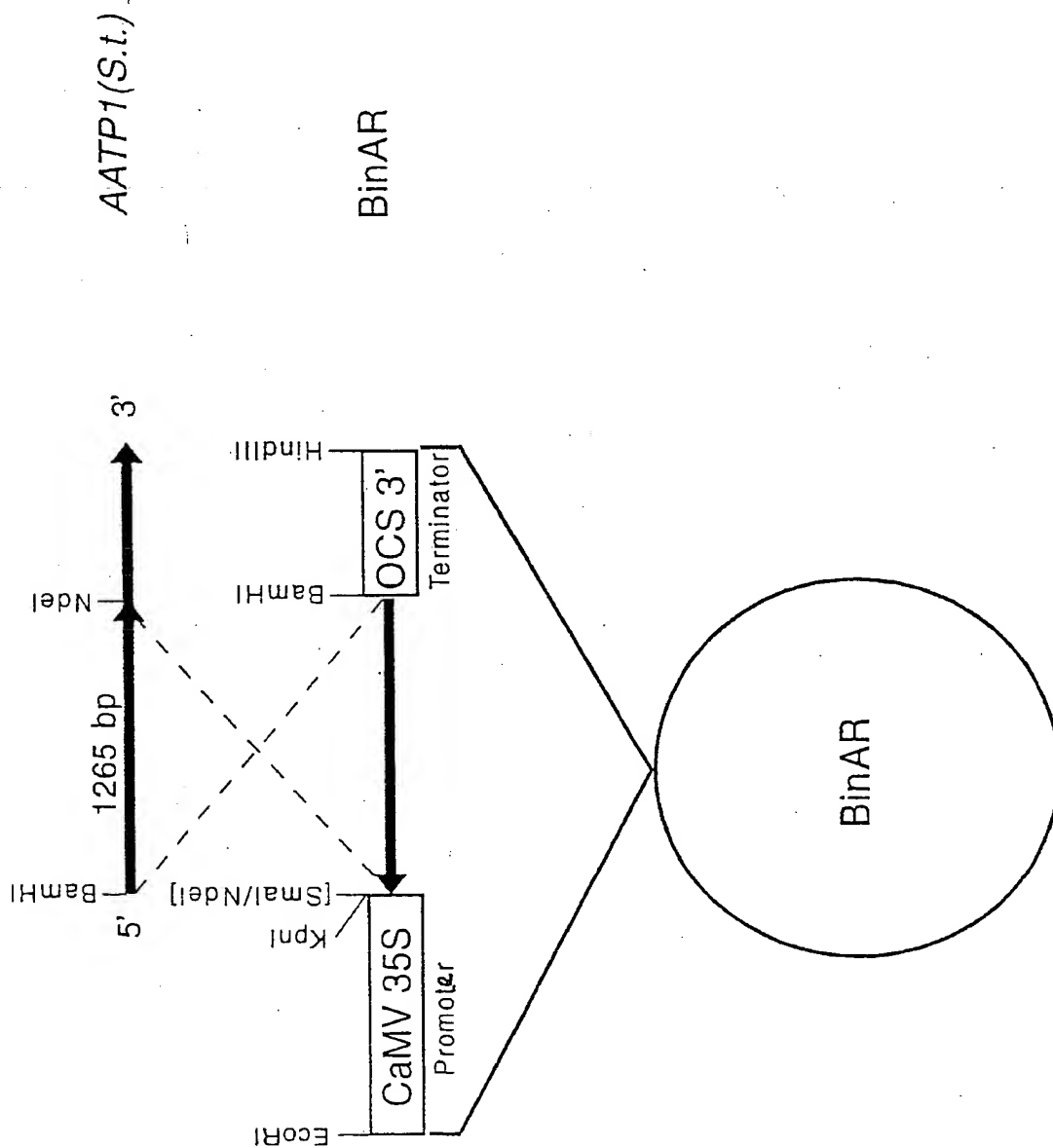
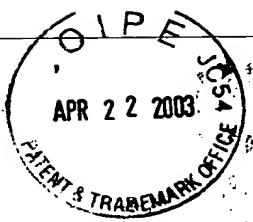


Fig. 2



DC Alignment:

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- 1 AATP1_A.T._
- 2 AATP2_A.t._
- 3 TLC_

10 20 30 40 50 60
1 MEAVIQTRGLLSLPTKPIGVRSQ LQPSHGLKQRLFAAKPRNLHGCLYPLTGTRNFKPLSQ 60
2 MEGLIQTRGILSLPASHR-SEKVLQPSHGLKQRLFTTN--LPALSLSLMVTRNFKPFSK 56
3 -----MS-----TSK-----SENY--LS- 11

70 80 90 100 110 120
1 PCMGFRFPTKREAPSSYARRRRGCWRRSCLRRSDSAAVVASRKIFGVEVATLKKIPLGL 120
2 SHLGFRFPTRREAEDSLARRKLRPRRKCVDEGDTAAMAVSPKIFGVEVTTLKKIVPLGL 116
3 -----EL-----RKIIWP-----IEQYENKKFLPLAF 33

130 140 150 160 170 180
1 MFFCILFNITILRDTKDVLVVTAKGSSAEIIFLKTWVNLPMAGFMILLYTKLSNVLSKK 180
2 MFFCILFNITILRDTKDVLVVTAKGSSAEIIFLKTWVNLPMAGFMILLYTKLSNVLSKK 176
3 MMFCILLNYSTLRSIKDGFVVDIG-T-ESISFLKTYIVLPSAVIAMIIYVKLCDILKQE 91

190 200 210 220 230 240
1 ALFYTVIVPFITYFGGFGFVMYPLSNYHPEALADKLLTTLGPRFMGPAILRIWSFCLF 240
2 ALFYTVIVPFIVYFGAFGFVMYPRSNLIQPEALADKLLATLGPFRMGPLAIMRIWSFCLF 236
3 NVFYVITSFFLGYFALFAFVLYPYDLPVHPDHKTIESLSLAYPNFKWFKIVGKWSFASF 151

250 260 270 280 290 300
1 YVMAELWGSVVSVLFWGFGANQITTVDEAKKFYPLFGIGANVALIFSGRTVKYFSNLRKN 300
2 YVMAELWGSVVSVLFWGFGANQITTVDEAKKFYPLFGLGANVALIFSGRTVKYFSNMRKN 296
3 YTIAELWGTMMLSLLFWQFANQITKIAEAKRFYSMFGILLANLALPVTSVVIGYFLHEKTQ 211

310 320 330 340 350 360
1 LGPGVDGSFV--ESHDEHCGNGTRICLSIGGSNRYV---P-L--PTRSKNKKEKPKMGT 352
2 LGPGVDGWAVSLKAMMSIVVGMGLAICFLYWWVNRYV---P-L--PTRSKKKVKPQMGT 350
3 I-VAEHLKFV---PLFVIMITSSFLIILTYRWMKNVLTDPRLYDPALVKEKKTAKLSF 267

370 380 390 400 410 420
1 MESLKFLVSSPYIRDLATLVVAYGISINLVEVTWKSCLKAQFPPSPNEYSAFMGAFSTCTG 412
2 MESLKFLVSSPYIRDLATLVVAYGISINLVEVTWKSCLKSQFPPSPNEYSAFMGDFSTCTG 410
3 IESLKMIFTSKYVGYIALIIAYGVSVNLEGVWKS VKELYPTKEAYTIYMGQFQFYQG 327

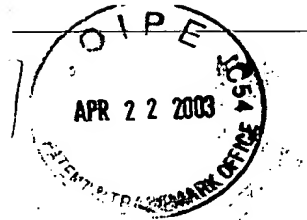
430 440 450 460 470 480
1 VATFTMMLLSQYVFNKYGWGVAAKITPTVLLLTGVAFSSLILFGGPFA-PLVAKLGMTPL 471
2 LATFTMMLLSQYVFNKYGWGVAAKITPTVLLLTGVAFSSLILFGGPFA-PLVAKLGMTPL 469
3 WVALAFMLIGSNILRKVSWLTAAMITPLMMFITGAFFSFIFFDSVIAMNLTGILASSPL 387

490 500 510 520 530 540
1 LAAVYVGALQNIIFSK-SAKYSLFDPCKEMAYIPLDEDTKVKGKAAIDVVCNPLGKSGGAL 530
2 LAAVYVPEVSSARVQVQHSSTPSAMQECLYPLDEVSKVKAKLQL-MWSATIGKSGGAL 528
3 TLAVMIGMIQNVLSK-GVKYSLFDATKNMAYIPLDKDLRVKGQA AVEVIGGRLGKSGGAI 446

550 560 570 580 590 600
1 IQQ-FMIL--SFGSLANSTPYLGMILLVIVTAWLAAAKSLEGQFNSLRLKSLRRKWREL 587
2 IQQ-FMIL--TFGSLANSTPYLGVILLGVITAWLAAAKSLEGPV----- 569
3 IQSTFFILFPVFGFI-EATPYFASIFFIIVILWIFAVKGLNKEYQVL-VNKNEK----- 498

- 1 HR 589
- 2 -- 569
- 3 -- 498

Fig. 3



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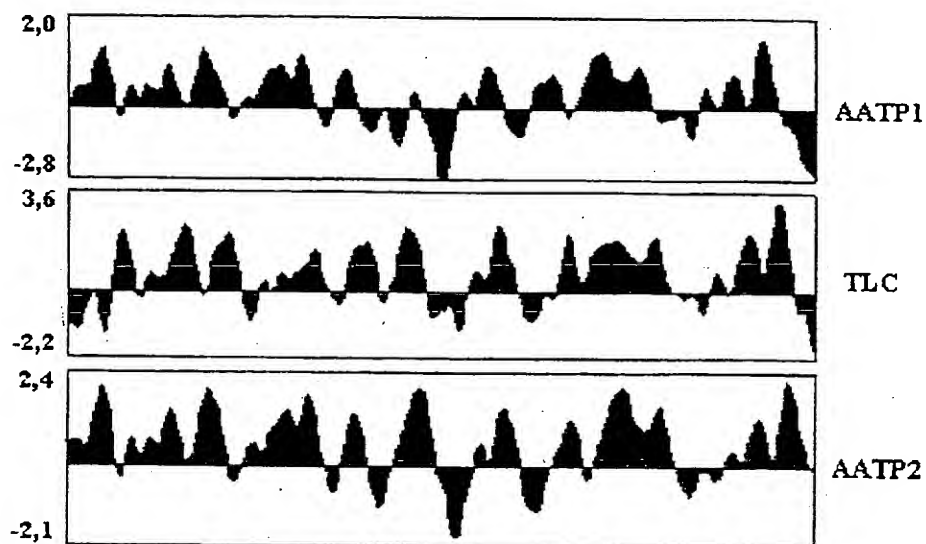
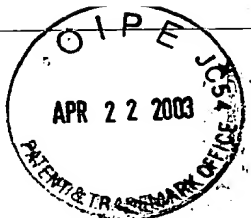


Fig. 4



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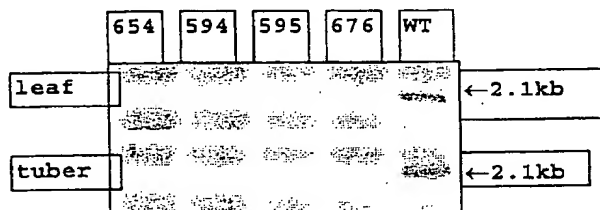


Fig. 5

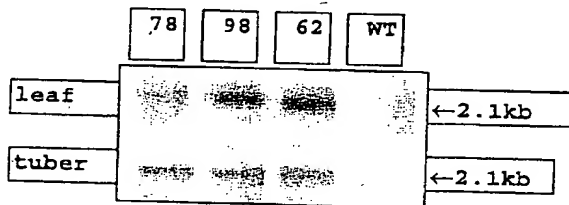


Fig. 6

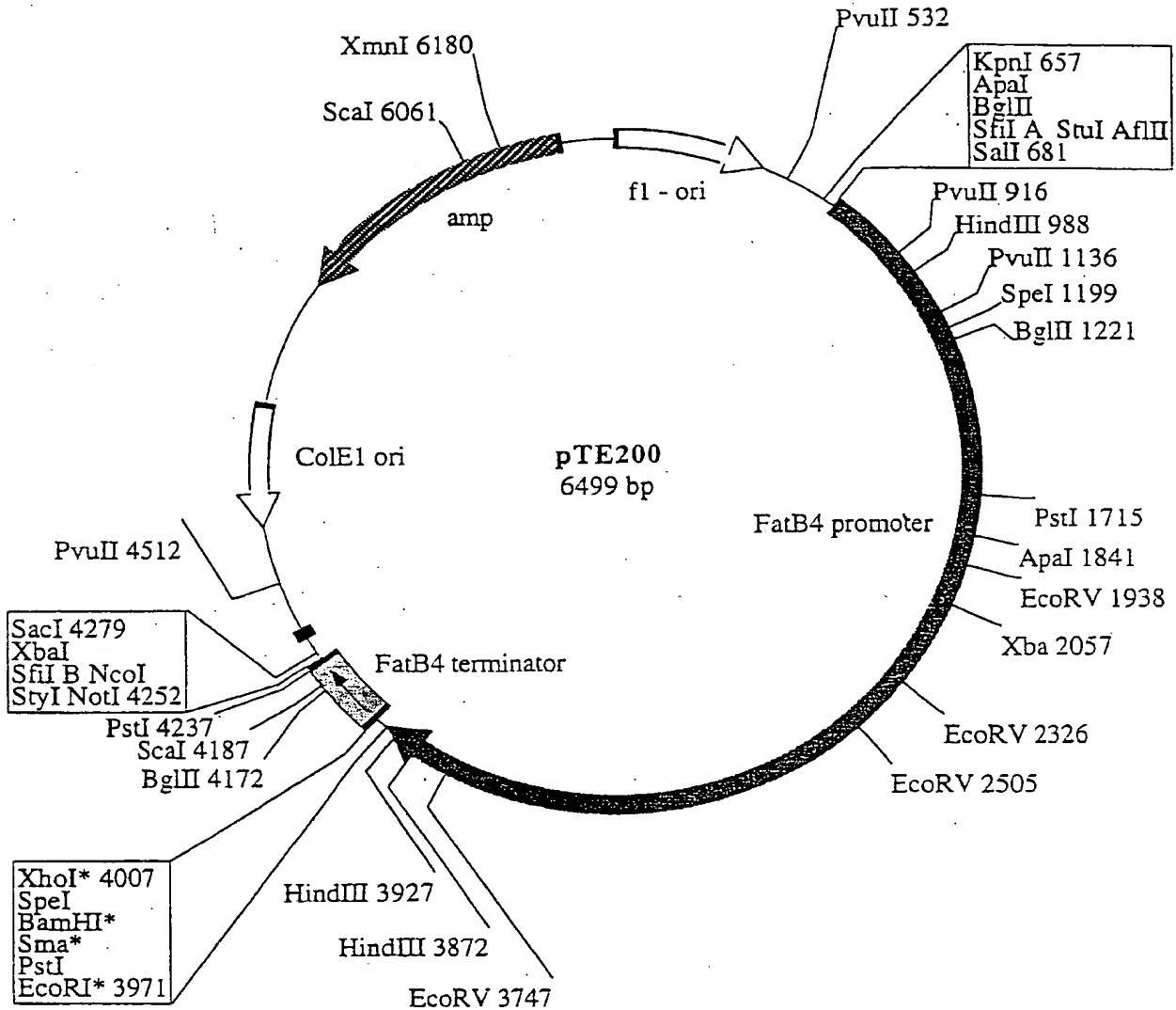


Fig. 7

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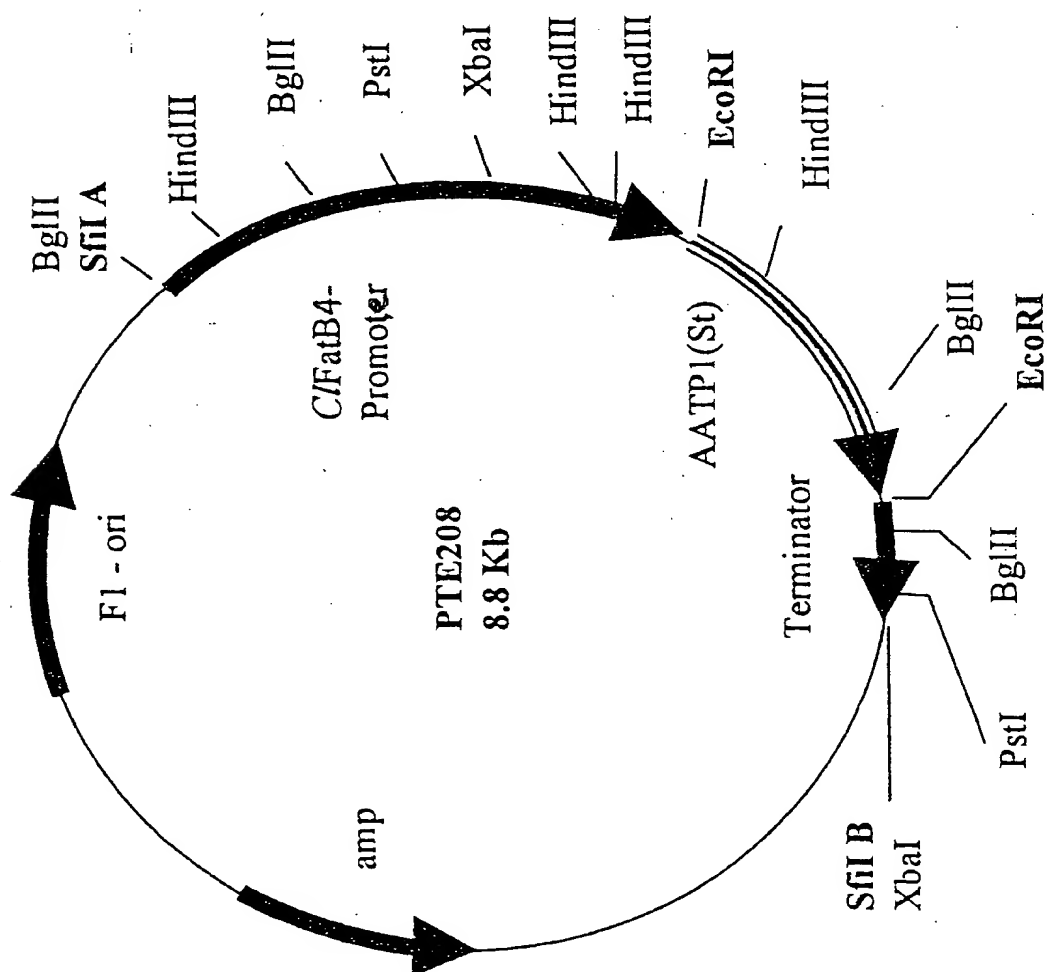


Fig. 8

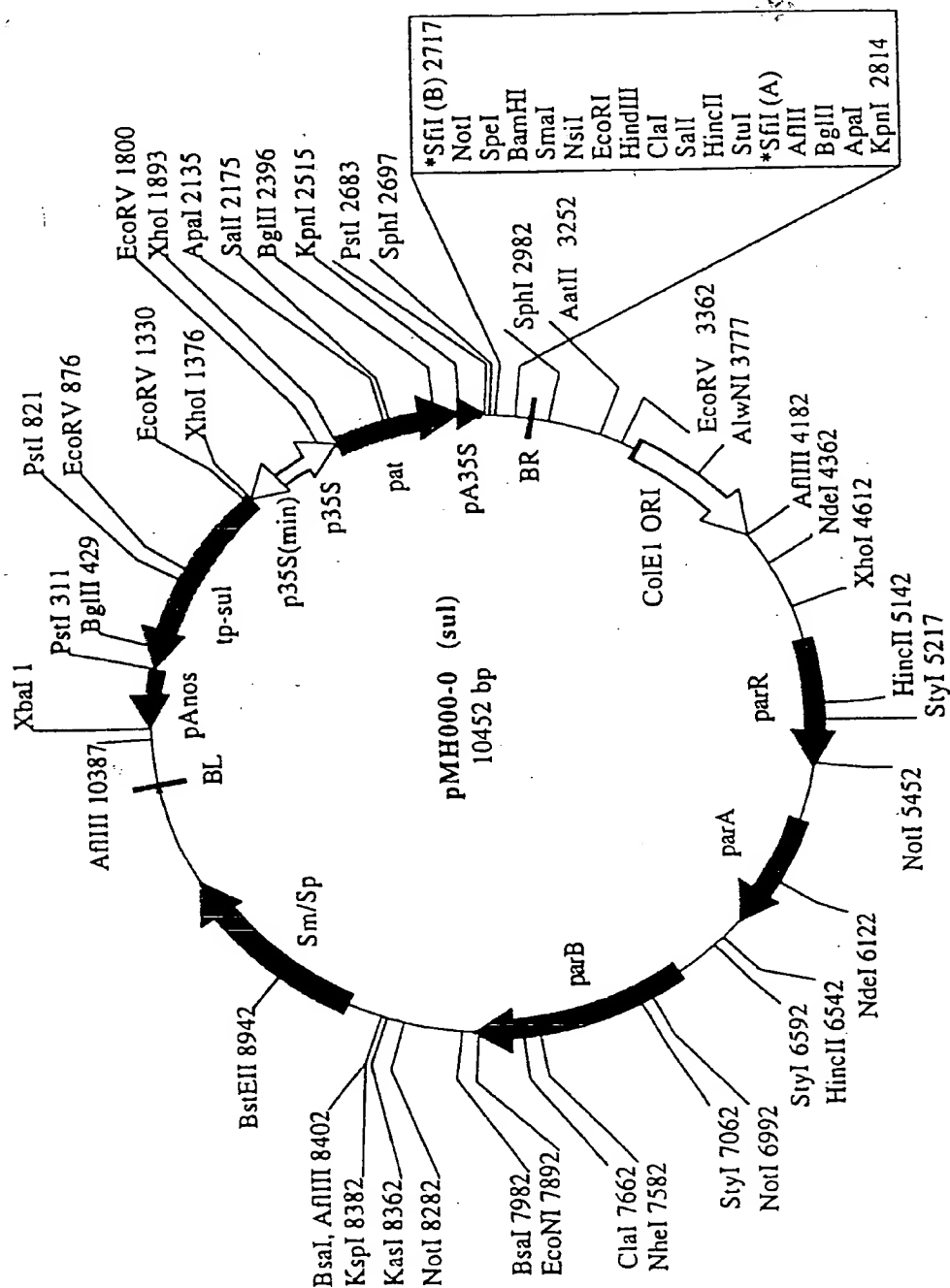


Fig. 9